

FIGURE 1

1 CACCACCTTC ACCTGGCTCG GGATTCTCAG CTCATGACG GTTCCAGCCA CTCTCGGCA GGGCGGGTGA GAGCGGGAC GGGCGCTCTC CAACCTGGCTG
 GTCCGTGAG TGGAGCCAGC CCTAAGAGTC CAGTACTTTC CAGGCTCGGT GGAGCGCGGT CCGCGCCCTG CCGCGGACAG GTTACCGAC

101 TGGGCTCTTG AACCGGAGC ATGGCAGAC AGGGGGGAT GGGCGCTTT GGGCGCTTT GGGCGCTTT GGGCGCTTT GGGCGCTTT GGGCGCTTT GGGCGCTTT
 ACCCGAGAC TTTCGGCTCG TACCTGTCG TGGCGGCTA CCGCGGCA CCGCGGCA CCGCGGCA CCGCGGCA CCGCGGCA CCGCGGCA CCGCGGCA CCGCGGCA
 1 M A Q H G A M G A F R A L C G L A L L C A L S L G Q R
 "MET"

201 CCCCACCGG GGTCCCGGT GCGCGCTCG GCGCGCTCG CTTCGAGCG GAGCGAGC GGGCTCTCG CCGCTTACA CAGCGCTCG CTCCCGCAT
 GGGCTGCGC CAGCGGCA CCGCGGAC CCGCGGAC GAGCGTTC CTTCCTCG CCGCGAGC GCGCGAGC GCGCGAGC GCGCGAGC GCGCGAGC GCGCGAGC
 28 P T G G P G C G P G R L L L G T G T D A R C C R V H T T R C C R D

301 TACCGCGCG AGGAGTCTG TTCCGAGTGG GAGCGATGT GTTCGAGC GTTCGAGC TGAATTCAG TCGGAGAC CTTCCTTAC GACCTGCGC CACCACTTT
 ATGGCGCGC TCTTCAGAC AAGCTTACC CTGAGTACA CAGCGTGG ACTTAACTG AGCGCTTGG GAGCGAGC CTTCGAGCCTG GTTCGAGCCTG
 61 Y P G E E C C S E W D C H C V Q P E F H C G D P C C T T C R H H P C

401 GTCCCGCAG CAGCGGTA CAGTCCAG GGAATTCAG TTTCCTTTC CAGTATAG ACTTCTTC GGGGAGCTTC TCGCGGCGC ACMAAGGCA
 CAGCGCTTC GGTCCCGCAT GTCCGCTTC CTTCATAGT AAGCGGAG GTCCATAG TACAGCGAG CCGCGGAG CCGCGGAG CCGCGGAG CCGCGGAG CCGCGGAG
 95 P P G Q G V Q S Q G K F S F G F Q C I D C A S G T F S O G H E G H
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501 CTCGAACT TCGAGACT GAGCGATTT CCGCTTCTC ACTGTTTC CTTCGAGCA GAGCGAGC GTTCGTGCG TCGCGGCTC CCGCGGCGC
 GAGCTTTTGA ACTGCTGA CTTCGCTGA GCGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC
 128 C K P W T D C T Q F G F L T V F P Q N K T H N A V C V P G S P P A
 "47365.Lm.p"

601 GAGCGCTTG GTTCCTGAC CCGCTCTC CTTCGCTCG CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC
 CTTCGAGC CAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC
 161 E P L G W L T V V L L A V A A C V L L L T S A Q L O L H I W Q L R S

701 GTTCAGTCA GTTCGCTGA GAGCGAGC TCTCTCTGA GTTCGCTCG CCGCGGCGC TCGCGGCGC TCGCGGCGC TCGCGGCGC TCGCGGCGC TCGCGGCGC
 CAGTCACTA CAGCGGCT CTTCGCTCG AGTCACTT CAGCGGCGC AGTCACTT TCTCTCTG TCTCTCTG TCTCTCTG TCTCTCTG TCTCTCTG TCTCTCTG
 195 Q C H W P R E T Q L L L E V P S T E D A R S C Q P E E R G E

801 GCGATCGCA GAGGAGAG GCGCGCTCG AGACTCTG GTTCAGCT GCGCGCTTC CCGCGGCGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC GAGCGAGC
 GGTAGCGT CTCTCTTTC CCGCGGCGC TCTGAGC CAGTCTGA CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC
 228 R S A E E K G R L G D L W V Q

901 CAGCGCGCA GGGGCTTTC GTTCGCTCT GGGCGGCGC CTCTCTCTT GCGCGGCGC GTTCGCTCT GCGCGGCGC GTTCGCTCT GCGCGGCGC GTTCGCTCT
 GTTCGCGCT CCGCGGCGC CAGAGAGCA CCGCGGCGC GAGCGAGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC CCGCGGCGC

1001 TCGAGTTC
 AGTCAAG

FIGURE 2

<241 aa, 1 stop
 <MW: 26000, pI: 6.34, NX(S/T): 1
 <greatest homology to MMU82534_1 glucocorticoid induced TNFR related>
 <protein - may be human homolog of this mouse gene>
 <25-26 potential signal peptide cleavage site>
 <33 4 TNFR - Cys repeat domains>
 <146 potential N-linked glycosylation site>
 <162 start potential transmembrane domain>
 <180 end potential transmembrane domain>
 < 1 10 20 30 40 50 60 70
 < MAQHGMGAFRALCGLALCALSLGQRPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYFGEECCSEW
 < 71 80 90 100 110 120 130 140
 < DCMCVQPEFHCGDPCCTTCRHHPCCPPGQGVQSQGKFSFGQCIDCASGTFSGHGHCXFWTDCYQGF
 < 141 150 160 170 180 190 200 210
 < TVFPGNKTNAVCPGSPPAEPLGWLTVVLLAAVACVLLTSAQLGHTWQLRSQCMWPRQTQLLEVP
 < 211 220 230 240
 < STEDARSCQFPEERGERSAEKGRLGLMW

FIGURE 3A

<consen01> 1 GGCACAGCACGGGGCGATGGGCGCGTTTCGGGGCCCTGTGCGGCCTGGCGC

<consen01> 51 TGCTGTGCGCGCTCAGCCTGGGTCAGCGCCCCACCGGGGT-CCCGGGTG

<consen01> 101 CGGCCCTGGGCGCCTCCTGCTTGGGACGGGAACGGACGCGCGCTGCTGCC

<consen01> 151 GGGTTCACACGACGCGCTGCTGCCGCGATTACCGGGCGAGGAGTGCTGT

<consen01> 201 TCCGAGTGGGACTGCATGTGTGTCCAGCCTGAATTCCACTGCGGAGACCC

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FIGURE 3B

<consen01> 251 TTGCTGCACGACCTGCCGGCACCACCCTTGTCCTCCAGGCCAGGGGGTAC

<consen01> 301 AGTCCCAGGGGAAATTCAGTTTGGCTTCCAGTGTATCGACTGTGCCTCG

<consen01> 351 GG-GACCTTCTCCGGGGGCCACGAAG--GCCACTGCAAACCTTGGACAGA

<consen01> 401 CTGCACCCAGTT-CGGG-TTCTCACTGTGTTCCCTGGGGAACAAGACCC

<consen01> 451 -ACAA-CGCTGTGTGCGTCCCAGGGTCCCCG-CCGGCAGAGCCGCTT-GG

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FIGURE 3C

<consen01> 501 GTGGCTGACCGTCGTCCTCCTGGCCGT-GGCCGCCTGCGTC-TCCTCCTG

<consen01> 551 ACCTCGGCCCAGCTTGGACTGCACATCTGGCAGCTGAGGAGTCAGTGCAT

<consen01> 601 GTGGCCCCGAGGTCTGTACAGCCTGGTGCGGGGAGGTGGGAGCATGGCT

<consen01> 651 GCCTGCTGACCGTGGCCCCCTGCATAGACCCAGCTGCTGCTGGAGGTGC

<consen01> 701 CGCCGTCGACCGAAGACGCCAGAAGCTGCCAGTTCCCCGAGGAAGAGCGG

<consen01> 751 GGCGAGCGATCGGCAGAGGAGAAGGGGCGGCTGGGAGACCTGTGGGTGTG

<consen01> 801 AGCCTGGCTGTCTCCGGGGCCACCGACCGCAGCCAGCCCCTCCCCAGGA

<consen01> 851 GCTCCCCAGGCCGCGAGGGGCTCTGCGTTCTGCTCTGGGCCGGGCCCTGCT

<consen01> 901 CCCCTGGCAGCAGAAGTGGGTGCAGGAAGGTGGCAGTGACCAGCGCCCTG

<consen01> 951 GACCATGCAGTTC

094397.07400

FIGURE 4

1 14FACAGCAC GGGGCGATGG GCGCTTTTCG GCGCTGTGCG TGCTGTGCG GCTGAGCTG GCTGAGCGCC CCAACCGGCG TCCCGGCTGC
 1 CCGTGTGCTG CCGCGTAC CCGCGACG CCGGACCG ACACACCG CAGTGTGCG CAGTGTGCG GCTGAGCGCC CCAACCGGCG TCCCGGCTGC
 *44825.G1TR.f *orf
 *44825.f1
 101 GCGCTGTGCG GCGCTGTGCG TGCGACCGC AGGACCGC GCTGTGCG GCTGTGCG AGCGCTGCT GCGCGATTA CCGCGGCGAG GAGTGTGCT
 CCGGACCG CCGGACCG AGCGCTGCT TGCTGTGCG CAGACCGC CCGGATGCG TGCGACCG CCGCGTAT GCGCGCTGCT CCGGACCG
 29 G P G R L L L G T G T D A R C C R V H T T R C C R D Y P G E C C S
 *44825.p1
 201 CCGGATGCGA CCGGATGCT GTGAGCTG ATTTCCAGTG CCGGACCG TGCTGTGCG CCGGACCG CCGGCTTGT CCGGACCGC AGGCGGTACA
 GCGTACCGT GAGTACACA CAGTGTGCG TTAAGTGC GCGTGTGCG AGGAGTGT GAGGCGCT GAGGCGCT GAGGCGCT GAGGCGCT TCCCGGCTG
 63 E W D C M C V Q P E F H C G D P C C T T C R H H P C P P G Q G V Q
 301 GTCGACCGG AATTCAGTT TTGCTTCCA GTGTATGCG TTGCTTCCA GAGCTTCT GCGGCGCGC GAGGCGCT GCGGACCGT GCGGACCGT GCGGACCGT
 CAGGTCGCC TTATAGTCA AACCGAGGT CACATAGCT ACAGGAGCG CCGGACCG GCGGCGCGT GCGGCGCGT GCGGCGCGT GCGGCGCGT GCGGCGCGT
 96 S Q G K F S P G P Q C I D C A S G T F S G G H E G H C K P M T D C
 *44825.G1TR.f
 401 ACCGATGCG GCTGTGCG TGCTGTGCG GCGGACCG AGGACCGC CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG
 TGCTGTGCG CCGGACCG AGGACCGC CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG
 129 T Q P G P L T V F P G E Q D P Q R C V R F R V P A G R A A M V A D R
 501 GTCGACCG GCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG
 CAGGACCG AGGACCGC CCGGACCG AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC
 163 R P P G R G R L R L L L T S A Q L G L H I W Q L R S Q C M W P R G
 601 TGCTGTGCG GAGGATGCG GAGGATGCG GAGGATGCG GAGGATGCG GAGGATGCG GAGGATGCG GAGGATGCG GAGGATGCG GAGGATGCG
 AGGACCGC GAGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG CCGGACCG
 196 L S Q P G A G R W E H G C L L T V A P L H R P S C C M R C R A R P
 701 AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC
 TTGTCGCTG TTGTCGCTG AGGACCGC TTGTCGCTG TTGTCGCTG TTGTCGCTG TTGTCGCTG TTGTCGCTG TTGTCGCTG TTGTCGCTG
 229 K T P E A A S S P R K S G A S D R Q R R R G G W E T C G C E P G C P
 801 CCGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC
 GAGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC AGGACCGC
 263 P G P P T A A S P S P G A P Q A A G A L R S A L G R A L L P W Q Q
 *44825.f2
 901 GAGTGTGCG CAGGATGCG GAGTGTGCG GAGTGTGCG GAGTGTGCG GAGTGTGCG GAGTGTGCG GAGTGTGCG GAGTGTGCG GAGTGTGCG
 CCGGACCGC CCGGACCGC CCGGACCGC CCGGACCGC CCGGACCGC CCGGACCGC CCGGACCGC CCGGACCGC CCGGACCGC CCGGACCGC
 296 K W V Q E G G S D Q R P G P C S S X A G X A
 *44825.f1

Fig. 5A

1 CAGCTCTCAT TTCTCCAAA ATCTGTTTGA GCCACTTGA AATATGCTT TTAAGCCATT CAACAACCTA AGGAGCTCAG AGATCATCTT GGAAGCTGTG
 1 CTCGACAGTA AAGAGGTTT TACACAACT CCGTGAACCT TTATACCGA AATGCGTAA GTTCTGAGT TCCTGAGTC TCTAGTAGA CCTCGACAC
 MetCysLeus erHisLeuG1 uasnMetPro leuserHis erArgThrG1 nGlyAlaGln ArgSerSert rPlysLeuTrp
 101 GCTCTTTTGC TCAATAGTTA TCTTGCTATT TCTTGCTCC TCCAGTTGCG TAATCTTTAT TTTCTCCAA TTAGAGACTG CTAGGAGGCC CTGATATGGCT
 28 CGAGAAAACG AGTTATCAAT ACAACGATAA AGAACGAGG AACTCAACCG ATTAGAAATA AAAAGAGGT AATCTCTGAC GATTCCTCGG CACATACCGA
 LeuPheCys SerIleValM etLeuLeuPh eLeuCysSer PheSerTrpL euilePheI1 ePheLeuGln LeuGluThra laLysGluPr ocysMetala
 201 AAGTTTGGAC CATTACCTC AATACGCTC AATATGGCAA ATGGCATCTT CTGAACCTCC TTGCGTAAAT AAGCTGTCTG ACTGGAAGCT GGAGATACCT CAGAAATGGCT
 TTCAAAACCTG GTAAATGGAG TTTTACCGTT TACGCTAGAA GACTTGGAGG AAGCGACTTA TTCCACAGAC TCACCTTCCA CCTCTATGAA GTCTTACCGA
 61 LysPheGlyp roLeuProSe rLysTrpGln MetalaSerS erGluProPr ocysValasn LysValsera sptPlysLe uGluileLeu GlnasnGlyLeu
 301 TATATTTAAT TTATGGCAA GTGGCTCCCA ATGCAAACTA CAATGATGTA CCTCTTTTTC AGCTCGGCT CTATAAAAAC AAAGACATGA TACAAACTCT
 ATATAAATTA AATACCGGTT CACCGAGGTT TACGTTTCAAT GTTACTACAT CCAGGAAAC TCCACGCCGA CATATTTTTC TTTCTGACT ATCTTTGACA
 95 TyrLeuI1 eTyrGlyGln ValalaProA snalaasnTy rAsnaspVal alaProPheC luValargLe uTyrLysasn LysaspMetI lecInThrLeu
 401 AACAAACAAA TCTAAATCC AATATGAGG AGGACTTAT GAATTCGATG TTGGGACAC CATAGACTTG ATATTCAACT CTGAGCATCA GGTCTTAAAA
 TTGTTTGTTC ACATTTTAGG TTTTACATCC TCCCTGAATA CTTAAGCTAC AACCCCTGTC GTATCTGAAC TATAAGTTGA GACTCGTAGT CCAAGATTTT
 128 ThrAsnLys SerLysileG lnaasnValG1 yGlyThrTy: GluLeuHisv alGlyaspTh rIleaspLeu IlePheAsns erGluHisG1 nValleuLys
 501 AATAAATACAT ACTGGGGTAT CATTTTACTA GCAATCCCG: AATTCATCTC CTAGACACTT GATTTGATCT CCTCATTTCC TTACAGCACAT GTAGAGGTGC
 TTATATGTA TGACCCCAT GTAATATGAT CGTTAGGGG TTAAGTAGAG GATCTGTGAA CTAAACTAGA GGAGTRAGG AGTCTGCTGA CATCTCCACG
 161 AsnAsnThrT yTrpGlyI1 eileLeuLeu AlaasnProG lnPheilese rAH
 601 CAGTGGGTGG ATTGGAGGGA GAAGATATT CTTCATATAA GTTGTCTGT CTACAAAAT CAACACAAAC AGAATCTCTC TGTGAGGAG ACCTGCACCTT AATAGTAGAT
 GTCACCCACC TAACTCCCT CTTCATATAA GTTGTCTGT CTACAAAAT CAACACAAAC AGAATCTCTC TGTGAGGAG ACCTGCACCTT AATAGTAGAT
 701 TCATGCCCTAT CTGAAGAGA CTCAGGGGAA GAGCCAAAGA CTTTGTCTG GATCTGCAGA AATCTTCTAT TAATCCATGA TAAACAAAT ATGCGATGACA
 AGTAGCGGATA GACTTTCTCT GAGTCCCTT CTGCGTTTCT CAAGACCAAC CTAGACCTCT TTATGAAGTA ATTAGGTACT ATTTGTTTA TACCTACTGT
 801 GAGCACATGT GCTTTTCAA GAATCTTTAT CTAACTCTG AATTCATGAG TGGAAAATG GAGTCTTATT CCCATGGAG ATTTACCTGG TATGCAAAAA
 CTCCTGTACA CGAAAGTTT CTTAGAAATA GATTAAGAAC TTAAGTACTC ACCTTTTAC CTCAGATAA GGGTACCTTC TAAATGGACC ATACGTTTTT
 901 GATCTGCGG CAGTAGCCCTG CTTTGTCTCT CATATTTCTT GCGTCTGTA ATTCATCTCT CTCACTCTCC CATCTTCTGA GACCTCCCA ATAAAAAGTA
 CCTAGACCCC CTCATCGGAC CGAAACAAGA GTATAAGAA GTATAGCAAT TNACTAAGAA GAGTATGAGG CTGAGAGACT CTGGGAGGGT TATTTTTCAT
 1001 GACTGATAGG ATGGCCACAG ATATGCCCTAC CATACCTTAC TTTAGATATG GTGCTGTTAG AGATAAAGA ACAATCTGAG AACTATTGGA ATAGAGGTAC
 CTCACATATCC TACCGGTGTC TATACGGATG CTATGGGAT: AATCTATAC CACCACAATC TTCTATTCT TCTTAGACTC TTGATAACCT TATCTCCATG

Fig. 5B

1101 AAGTGCATA AATGGAATG TAGCTATCT GGAATTTCT CTGGTTTTA TCTTCTCAG GATGAGGGT GCCTTAAAA GCCTATCAA AGGACTCAT
 TACACCTAT TTTACCTTAC ATCGGATAGA CCTTTAAGA GAACCAAAAT ACAAGGAGT CTACCTCCA CGAAATTTT CGGAATAGT TCTCAGTAA

1201 CGCAACCTC AGTAGAGCT TTTGAGACC TTACTGTTC TAACATTGC TAATGTAA GAAGACTAA CCATTAGTAA TCATTAGGTT
 GCCTTGGAG TGCATCTCGA AACACTCTGG AATGACAAC ACACACAG ATTGTAAAG ATTACTATT CTCTCTATT CTTTCTCAT AGTAATCCAA

1301 TAAACCCAGA ATGGTATTAT CATTACTCGA TTATGCTAT TAATGATTTA GTATTTTAG CTAGCTTCC ACAGTTTGA AAGTGTCTT GTAAACAGT
 ATTGGGGTCT TACCATAATA GTAAATGACCT AATACAGTAC ATTACTAAT CATAAATC GATCGAAGG TGTCAAAGT TTCACGAAG CATTGTGCA

1401 TAGCAATTT ATGAAGTTAA TTGGGAGGC ATTTGGGGA AATTTTATG GATGAGATG TGATAGCATA GATAGCCAA CTTTCTCAA CTCAATAGGAC
 ATCGTTAAGA TACTTCAATT AACCGTCCG TAAACCCCT TTTAAATCA CTACTTTAC ACTATCGTAT CGTATCGGT GAAAGGAGT GAGTATCTC

1501 AAGTCACTAC AAGAGGCAAT GGTAGTCCC CTGCTTCCA CTCTCTCAG TTTAGAAATG TTTTCTTC TATCTCTTA TAAGACTTA AACCTAGG
 TTCACTGAT TTCTCCGTTA CCATCAGG GACCTAACGT GACAGAGTGG AATCTTAAC AATAAGAGG ATAGCACAAT ATTCTAGAT TTGAAATCGC

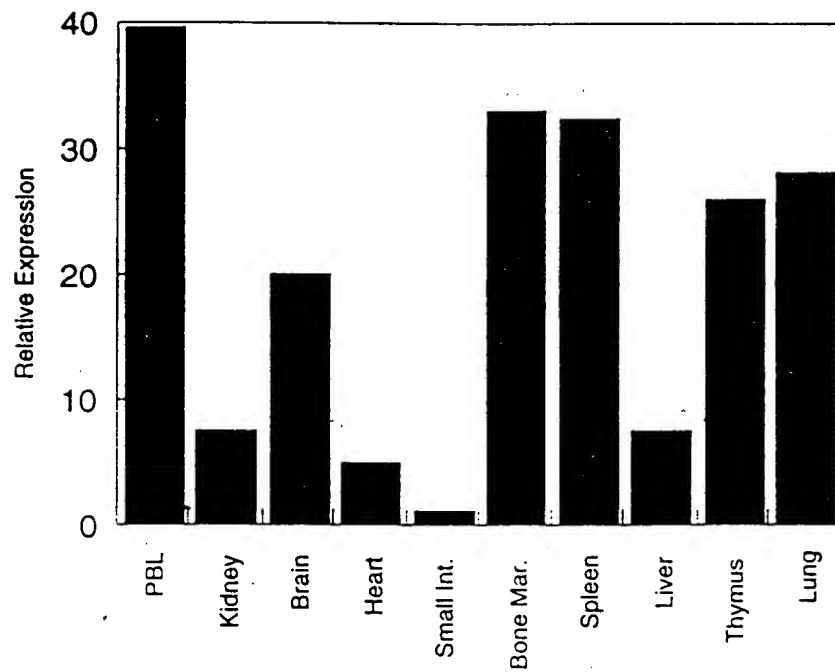
1601 AATTCACCTT TCAGGAAGCA TATTCCTCTT TAGCCCAAG TCAGCAGAGT GAAGCTCAA CAGATCTTTC CTTTACCAG ACCTTTTTT TTTTTTTTC
 TTAAGTAAA AGTCTCTCT ATAGGGGAA ATCGGTTCC ACTCTCTCA CTCTGATCTT GTCAGAAAG GAAATGCTG TGTAAAAA AAAAAAAG

1701 TGCTGAATC AGGAGATCC AGGATCTGT TCAGGCCAA TCCCAACCA ATTCCTCTT TCACCTTGA GGGCCATCT TAGTCAAATG TGCTAACTTC
 ACGGACTTAG TCCCTCTAGG TCCTAGACA AGTCCGGTT AGGTTGCTT TAAGGGAAA AGTCAAACT CCGGGTGA ATCACTTAC ACGATTGAAG

1801 TAAATAATA AATAGCACTA ATTCAAAT TTTCGAATCT TAAATAGCT ACTTCNGGT TCGTTCTGA AAGGATATA ATGATTACAT TGTAAACAA
 ATTTATTAT TTATCTGAT TAAGTTTAA AACCTTGA ATTTAATCGA TGAACGCCA ACGAACACT TTCCNTATAT TACTAATCTA ACATTGTCT

1901 TTTAAAAAT TTATGGATAT TTGTAAAAG CTCATTATC TAAATAATA TTACATGTA AGCT
 AAATTTTATA AATACCTATA AACACTTTC GACCTAATAC AATTTATAT AATGATCAT TCGA

Fig. 6

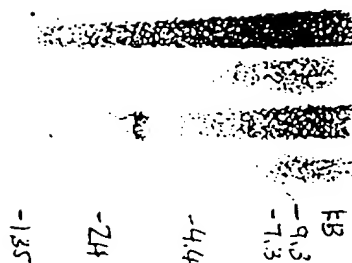


00760 2557960

Cell Type	Stimulus	Relative mRNA expression (approx.)
T cells	(-)	1
	anti-CD3	77
	PHA	35
Monocytes	(-)	14
	LPS	23

Fig. 7

Fetal
Human



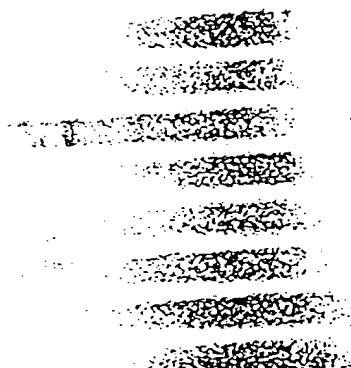
Kidney
Liver
Lung
Brain

Human
Adult



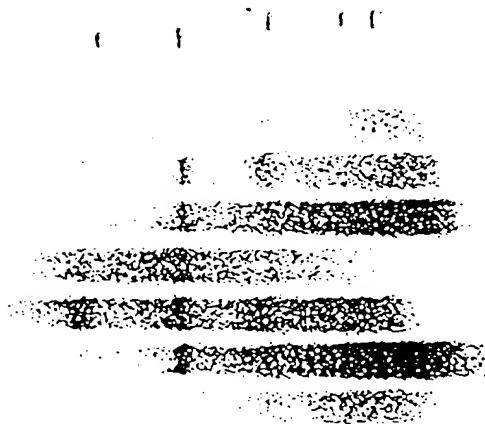
Pancreas
Kidney
Sk. Muscle
Liver
Lung
Placenta
Brain
Heart

Human
Adult



PBL
COLON
SM. INTEST
OVARY
Testis
prostate
Thymus
Spleen

Cancer



G-361
A549
SW480
Raji
MOLT-4
K-562
Hela S3
HL-60

Fig. 8

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001397.01100

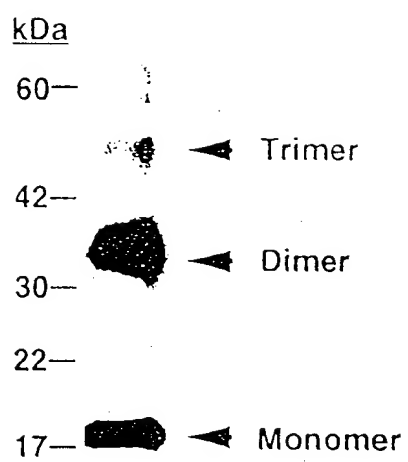


Fig. 9

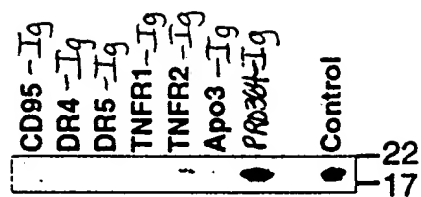


Fig. 10

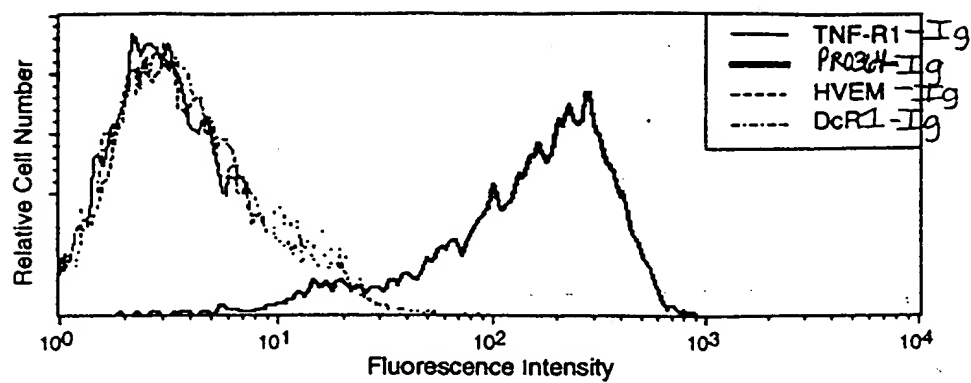


Fig. 11A

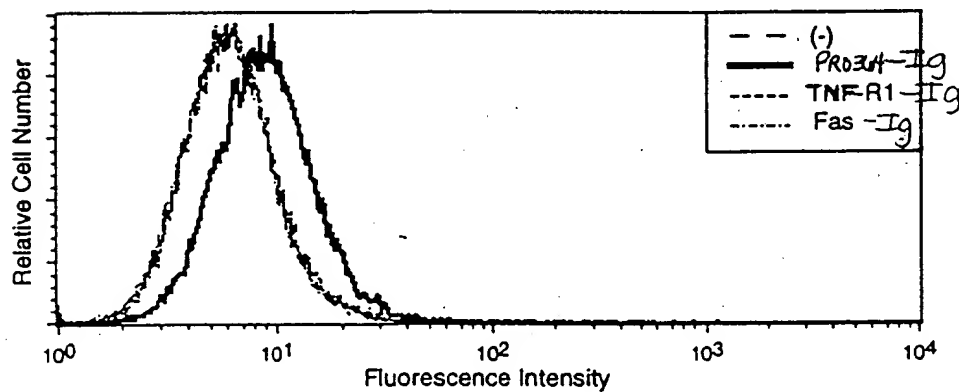


Fig. 11B

001120-2465T950

glt^r TNF H10g
PIN192

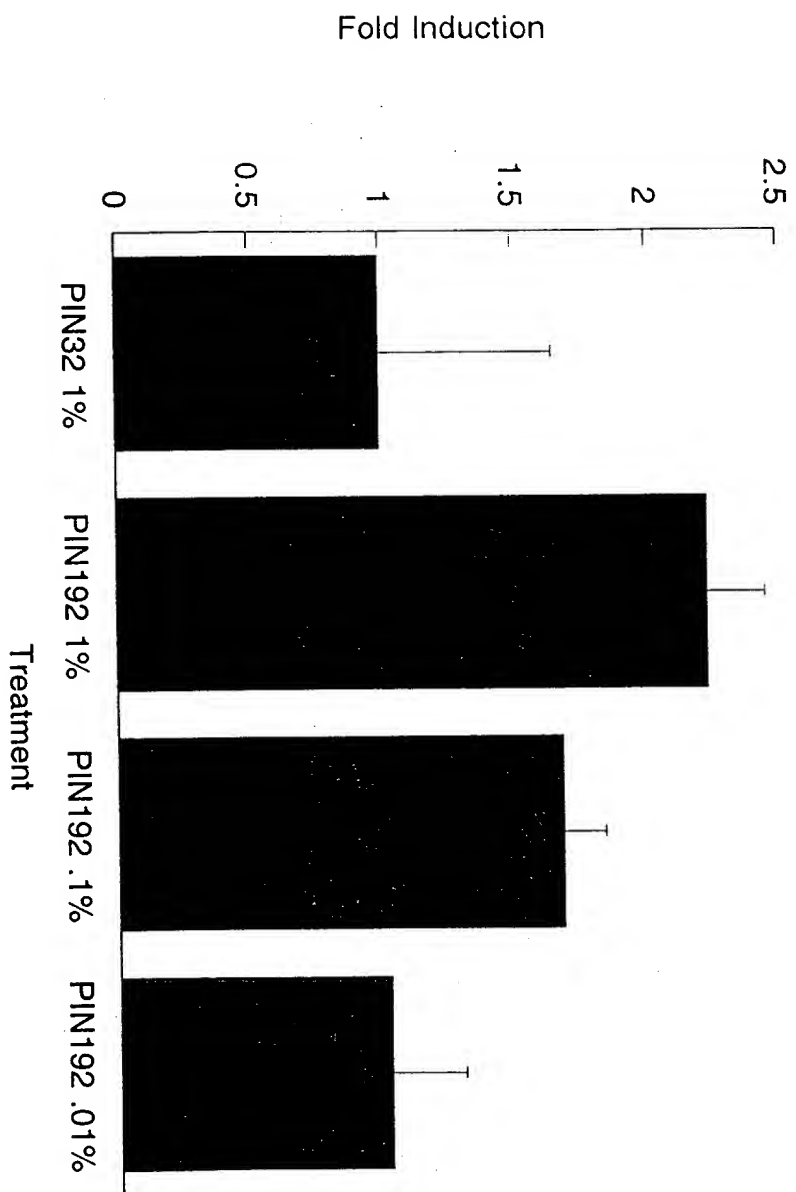


FIG. 12

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